

Table S1. Mutations, corresponding amino acid and point accepted mutation (PAM) of the glycoprotein Gc coding region in the mutant spectra RVFV subjected to four passages in the absence or presence of 40 μ M Favipiravir (T-705)

No drug			40 μ M favipiravir		
Mutation ^a	Amino acid substitution	PAM250 ^b	Mutation ^a	Amino acid substitution	PAM250 ^b
G2073A (8)	-	-	G2045A	S698N	1
T2079C (8)	-	-	C2046T	-	
A2094G (7)	-	-	C2055T	-	
G2112A (7)	-	-	A2056C	T702P	0
A2148G (8)	-	-	C2057T	T702I	0
G2154A (8)	-	-	C2058T	-	
T2172C (8)	-	-	C2060T	T703I	0
A2181G (8)	-	-	G2063A	C704Y	0
C2184T (8)	-	-	C2064T	-	
C2259T (9)	-	-	C2066T	S705F	-3
C2283T	-	-	G2073A (4)	-	
T2292C (9)	-	-	G2077A	V709I	4
A2295G (9)	-	-	T2079C (4)	-	
G2328A (9)	-	-	C2082T	-	
T2340C (8)	-	-	A2083C	T711P	0
G2349A (8)	-	-	G2088A	-	
A2382G (8)	-	-	A2094G (4)	-	
T2388C (8)	-	-	G2097A	-	
G2418A (7)	-	-	C2103T	-	
C2427T (6)	-	-	C2105T	T718I	0
C2466T (6)	-	-	T2111C	L720S	-3
T2478C (6)	-	-	G2112A (5)	-	
T2502C (6)	-	-	G2131A	G727R	-3
C2514T (6)	-	-	G2133A	-	
G2531C (6)	S860T	1	C2141T	A730V	0
C2541T (6)	-	-	T2145C	-	
A2544T (6)	-	-	A2148G (4)	-	
T2575C (7)	-	-	G2154A (5)	-	
T2640C (8)	-	-	G2160A	-	
T2655C (8)	-	-	T2172C (3)	-	
T2664C (7)	-	-	A2181G (3)	-	
T2754C (8)	-	-	C2184T (3)	-	
C2759T (3)	S936L	-3	G2219A	C756Y	0
G2763A (6)	-	-	G2223A	-	
C2766T (6)	-	-	G2227A	G759S	1

C2808T (8)	-	-	C2229T	-	
C2814T (8)	-	-	C2259T (6)	-	
A2838G (7)	-	-	C2271T	-	
T2868C (7)	-	-	T2292C (6)	-	
T2889C (8)	-	-	A2295G (6)	-	
G2911A	E987K	0	G2307A	-	
A2913C (9)	E987D	3	T2320C	S790P	1
A2933G (2)	K994R	3	G2325A	W791STOP	
A2976G (9)	-	-	G2328A (6)	-	
T2988A (10)	-	-	T2340C (6)	-	
C3030T (7)	-	-	C2345T	A798V	0
A3033G (7)	-	-	G2349A (5)	-	
C3057T (7)	-	-	G2359A	V803I	4
T3075C (8)	-	-	G2364A	-	
G3084A (8)	-	-	C2376T	-	
A3087G (8)	-	-	A2382G (4)	-	
G3093A (8)	-	-	G2385A	-	
C3096T (6)	-	-	T2388C (3)	-	
			G2403A	-	
			G2405A	C818Y	0
			G2416A	G822R	-3
			G2418A (5)	-	
			G2424A	-	
			C2427T (4)	-	
			C2439T	-	
			G2457A	-	
			C2466T (4)	-	
			T2478C (5)	-	
			C2489T	A846V	0
			T2502C (5)	-	
			C2514T (5)	-	
			G2531C (5)	S860T	1
			C2533T	-	
			C2541T (6)	-	
			C2543T	T864I	0
			A2544T (6)	-	
			G2554A	G868S	1
			T2575C (8)	-	
			G2578A	G876R	-3
			C2592T	-	

			T2597C	F882S	-3
			C2600T	T883I	0
			C2604T	-	
			G2614A	V888I	4
			C2626T (2)	-	
			G2628A	-	
			C2633T	A894V	0
			T2640C (8)	-	
			T2655C (8)	-	
			C2663T	S904F	-3
			T2664C (8)	-	
			C2693T	A914V	0
			C2708T	P919L	-3
			C2714T	S921L	-3
			C2723T	P924L	-3
			G2727A	-	
			A2730G	-	
			G2731A	G927A	1
			C2736T	-	
			G2743A	E931K	0
			T2754C (6)	-	
			G2763A (6)	-	
			C2766T (6)	-	
			C2808T (6)	-	
			C2814T (6)	-	
			G2829A	M959I	2
			A2838G (7)	-	
			G2844A	-	
			C2847T	-	
			C2849T	T966I	0
			T2868C (7)	-	
			G2872A	V974I	4
			T2879C	F976S	-3
			G2881A (2)	E977K	0
			G2886A	-	
			G2888A	G979D	1
			T2889C (7)	-	
			G2906A	R985K	3
			G2907A	-	
			A2908G	N986D	2

			A2913C (7)	E987D	3
			C2918A	T989N	0
			C2924T	A991V	0
			G2935A	G995R	-3
			G2966A	G1005D	1
			A2976G (5)	-	
			T2988C	-	
			C2989T	-	
			T2988A (5)	-	
			G2998A	D1016N	2
			G3021A	-	
			C3030T (5)	-	
			A3033G (5)	-	
			G3038A	C1029Y	0
			A3054G	-	
			C3057T (5)	-	
			T3075C (4)	-	
			G3084A (4)	-	
			A3087G (4)	-	
			G3093A (4)	-	
			C3096T (4)	-	
			G3098A	C1049Y	0
			G3119A	G1056E	0

^aResidue numbering is according to RVFV strain SA-75, accession number DQ380189. The number of clones in which the mutation is found is given in parenthesis. Bold-face indicates mutations found only in absence (first column) or presence (fourth column) of favipiravir.

^bPAM250 is the amino acid substitution frequency score in which -7 represents minimum acceptability and +7 maximum acceptability, relative to random sequences (1)

References

1. Feng DF, Doolittle RF. 1996. Progressive alignment of amino acid sequences and construction of phylogenetic trees from them. *Methods in Enzymol* 266:368-82.